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Genetic diversity and its impact on yield related traits in potato

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Abstract

Potato is a tuberous crop, which is a good source of starch used as a dietary supplement and plays an important role in the Indian diet. Experiment was conducted in research cum instructional farm IGKV, Raipur (C.G.). The analysis of genetic variance revealed that there was significant genetic variability in the experimental materials. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) ranged from 24.76 to 6.90 and 25.29 to 11.2980, respectively. Highest GCV and PCV reported for Number of Compound leaves plant^{-1} (24.76, 25.29), Unmarketable tuber yield plant^{-1} (kg) (21.92, 22.895) and Fresh weight of shoot plant^{-1} (g) (20.454 21.011). High heritability coupled with high genetic advance was reported for number of total leaflets plant^{-1}, Marketable tuber yield plant^{-1}, Biological yield plant^{-1}, Number of Compound leaves plant^{-1}, Harvest index, Fresh weight of shoot plant^{-1}, Plant height at maturity, Tuber yield plant^{-1}, Plant emergence, Unmarketable tubers yield plant^{-1}, Dry weight of shoot plant^{-1} and Number of tubers plant^{-1} Indicated presence of additive gene action in these traits. Divergences analysis grouped these genotypes in to six clusters, the inter-cluster distance was a higher than intra-cluster distance suggesting wider genetic diversity among the genotypes of different groups. The highest intra-cluster value was maximum in cluster II (6.00) and minimum in cluster I (4.19). The highest inter-cluster distance was between cluster III and V (12.371) indicated maximum exploitation of heterosis on hybridization. Two characters number of compound leaves plant^{-1}and fresh weight of shoot plant^{-1} showed maximum contribution towards total divergences among different characters.

Keywords: Divergences, cluster, heritability and heterosis

Introduction

The potato (*S. tuberosum* L. 2n= 4x=48) is a crucial staple food and cash crop that was domesticated approximately 8,000 years ago in the Andes Mountains of South America (International Potato Centre, 2019) [7]. Globally, it ranks as the third most important food crop after rice and wheat in terms of human consumption. The potato has great potential for contributing to a sustainable food supply and is a vital option for food security in many developing nations. In India potato cultivated area, production and productivity is 2351.6 in ' 000 Hectare, 60540.2 MT and 25.7 in MT/Hectare respectively (2022-23). Uttar Pradesh is leading potato producing state followed by West Bengal, Bihar, Madhya Pradesh and Punjab. (Anonymous, 2023) [1].

The Potato is anon-woody (herbaceous) plant and grows habit varies between the species. The plant has a rosette or semi-rosette characteristics. Potato herbs are annual, biennial or perennial Sahair *et al.* (2019) [17]. Potatoes are one of the most vital staple crops worldwide, providing essential nutrition and serving as a significant source of income for millions of farmers. Despite their economic and nutritional importance, the potato is highly nutritious, containing 22% carbohydrates, 2% proteins, and 0.1% fats, along with 74% water. It is also rich in minerals and trace elements such as potassium, sodium, iodine, and magnesium, and provides essential nutrients like folic acid, pyridoxine, vitamin C, ascorbic acid, and iron (Sahar *et al.* 2017) [18]. The challenge of enhancing potato yield persists due to various biotic and abiotic stresses.

Genetic diversity within potato cultivars plays a crucial role in addressing these challenges by providing a pool of traits that can be harnessed to improve yield and resilience. Genetic diversity refers to the total number of genetic characteristics in the genetic makeup of a species.

It serves as the foundation for adaptive evolution and breeding, enabling plants to survive and thrive under changing environmental conditions. In potatoes, genetic diversity is not only essential for developing new varieties with higher yields but also for enhancing traits such as disease resistance, drought tolerance, and overall plant vigor.

Materials and Methods

The present investigation was conducted at Indira Gandhi Krishi Visvawidyalaya, Raipur (C.G.). This investigation comprising of 50 advanced breeding lines of potato genotypes with two cheek variety (kufri Surya and kufri jyoti) during *rabi* 2023. Genotypes were planted in RBD design with three replications. The genotypes were sown with 60 × 30 cm row to row and plant to plant spacing. Recommended cultural practices and plant protection measures followed to raise healthy crop five randomly selected competitive plants of each genotype of each replication were taken for recording observations on 15 morphological characters (table no. 1). The data on days to maturity was recorded on plot basis performances.

Table 1: Fifteen morphological characters used in experiment

S. N.	Characters
1	Plant emergence (%)
2	Number of shoots plant^{-1}
3	Number of branches plant^{-1}
4	Fresh weight of shoot plant^{-1} (g)
5	Dry weight of shoot plant^{-1} (g)
6	Number of compound leaves plant^{-1}
7	Number of total leaflets plant^{-1}
8	Plant height at maturity (cm)
9	Number of tubers plant^{-1}
10	Number of eyes tuber^{-1}
11	Unmarketable tuber yield plant^{-1} (kg)
12	Biological yield plant^{-1} (kg)
13	Harvest index (%)
14	Marketable tuber yield plant^{-1} (kg)
15	Tuber yield plant^{-1} (kg).

Analysis of variance was performed using Fisher's method. Genotypic variances ($\sigma^2 g$), phenotypic variances ($\sigma^2 p$), and environmental variances ($\sigma^2 e$) were calculated according to the procedures outlined by Burton and Devane (1953) [4]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was estimated according to Burton & Deyane (1953) [4]. Expected genetic advance for each character was calculated following the method described by Johanson *et al.*, (1955) [8]. The environment wise data was subjected to multivariate analysis as suggested by Mahalanobis (1936) [9] separately and genotypes were grouped in to different clusters following Tocher's method (Rao, 1952) [15] and character contribution towards diversity was estimated. Broad-sense heritability were estimated using the formula adopted by Falconer and Mackay (1996) [6] as follows:

$$H^2 = (\sigma p^2 / \sigma g^2) \times 100$$

Where: H^2= heritability in the broad sense, σg^2 = genotypic variance and σp^2 = phenotypic variance.

Table 2: Least of experimental materials

S. N.	Genotype	Genotypes code	Source	S. N.	Genotype	Genotypes code	Source
1	AICRP-P- P-78	G1	CPRI, Shimla	26	K. Neelkanth	G26	CPRI, Shimla
2	AICRP-P- C-6	G2	CPRI, Shimla	27	K. Khyati	G27	CPRI, Shimla
3	AICRP-P- P-48	G3	CPRI, Shimla	28	KCH-1	G28	CPRI, Shimla
4	AICRP-P- C-5	G4	CPRI, Shimla	29	KCH-3	G29	CPRI, Shimla
5	AICRP-P- C-13	G5	CPRI, Shimla	30	K.Himalini	G30	CPRI, Shimla
6	AICRP-P- P-42	G6	CPRI, Shimla	31	K. Ashoka	G31	CPRI, Shimla
7	AICRP-P- C-17	G7	CPRI, Shimla	32	K. Garima(MM-11)	G32	CPRI, Shimla
8	AICRP-P- C-20	G8	CPRI, Shimla	33	K. Arun	G33	CPRI, Shimla
9	AICRP-P- C-14	G9	CPRI, Shimla	34	K. Lalima (C-15)	G34	CPRI, Shimla
10	AICRP-P- P-85	G10	CPRI, Shimla	35	K. Lima	G35	CPRI, Shimla
11	2020 IGP - 1	G11	CPRI, Meerut	36	AICRP-P- 45	G36	CPRI, Shimla
12	2020 IGP - 2	G12	CPRI, Meerut	37	AICRP-P- 46	G37	CPRI, Shimla
13	2020 IGP - 3	G13	CPRI, Meerut	38	AICRP-P- 53	G38	CPRI, Shimla
14	2020 IGP - 4	G14	CPRI, Meerut	39	AICRP-P- 73	G39	CPRI, Shimla
15	2020 IGP - 5	G15	CPRI, Meerut	40	AICRP-P- 21	G40	CPRI, Shimla
16	2020 IGP - 6	G16	CPRI, Meerut	41	2022 IGP-1	G41	CPRI, Meerut
17	2020 IGP - 7	G17	CPRI, Meerut	42	2022 IGP-2	G42	CPRI, Meerut
18	2020 IGP - 8	G18	CPRI, Meerut	43	2022 IGP- 3	G43	CPRI, Meerut
19	2020 IGP - 9	G19	CPRI, Meerut	44	2022 IGP- 4	G44	CPRI, Meerut
20	2020 IGP - 10	G20	CPRI, Meerut	45	2022 IGP- 5	G45	CPRI, Meerut
21	K. Surya	G21	CPRI, Shimla	46	2022 IGP- 6	G46	CPRI, Meerut
22	K. Jyoti	G22	CPRI, Shimla	47	2022 IGP- 7	G47	CPRI, Meerut
23	K. Sinduri (P1)	G23	CPRI, Shimla	48	2022 IGP- 8	G48	CPRI, Meerut
24	K. Lalit	G24	CPRI, Shimla	49	2022 IGP- 9	G49	CPRI, Meerut
25	K. Mohan (RH-2)	G25	CPRI, Shimla	50	2022 IGP- 10	G50	CPRI, Meerut

Note: K. = Kufri, KCH= Kufri Chipsona, CPRI= Central Potato Research Institute

The analysis was performed by analytical software XLSTAT. 5.7 following mahalanobis distances using UPGA. The material utilized for experimentation is listed (Table no. 2) below

Results and Discussion

Genetic parameters

The present investigation was undertaken to estimate genetic variability, heritability, genetic advance and genetic divergences for important yield component characters among fifty genotypes of potato in a randomized block design with three replications during *rabi* seasons 2023. The results from these genetic parameter components indicate a substantial amount of genetic variability in the material currently under investigation. The genotypic coefficient of variation (GCV) ranged from 6.90 to 24.76% and phenotypic coefficient of variation (PCV) ranged from and 11.2980 to 25.29%, respectively (table no. 3). Sivasubramaniah and Menon (1973) [20] categorized GCV and PCV values as low (<10%), moderate (10-20), and high (>20%). Highest GCV and PCV reported for number of compound leaves plant^{-1} (24.76, 25.29), Unmarketable tuber yield plant^{-1} (kg) (21.92, 22.895) and fresh weight of shoot plant^{-1} (g) (20.454 21.011) respectively. Similar results were recorded by Ebrahim *et al.* (2020) [5] for Plant height, tuber yield plant^{-1}, marketable tuber yield and unmarketable tuber yield plant^{-1}. Basavaraja *et al.* (2005) [2] and Biswas *et al.* (2005) [3] for plant height; by Pradhan *et al.* (2014) [13]. The estimation of PCV if high than the estimation of GCV for almost all the character, some characters exhibit little differences between PCV and GCV it indicates that the environment has little influence on the expression of the character. Selection for improvement of such characters will be effective. However, if the GCV is less than the PCV, the apparent variation is influenced not only by the genotype but also by the environment.

Heritability

Heritability is a measure of the proportion of total phenotypic variation in a population that is attributable to genetic variation among individuals. It is often expressed as a percentage and provides an estimate of the degree to which a trait can be passed from parents to offspring. Genetic Advance refers to the expected improvement in a trait achieved through selection based on the heritability and the selection differential. It is the difference between the mean of the offspring of selected parents and the mean of the original population.

The heritability (table no. 3) percentage was categorized as low, moderate, or high based on the criteria suggested by Robinson and Callbeck (1955) [16]: 0-30% = Low, 30-60% = Moderate and > 60% = High. High heritability coupled with high genetic advance indicated presence of additive gene action in these traits. Number of total leaflets plant^{-1} (98, 25.329%), Marketable tuber yield plant^{-1} (kg) (97.83, 29.238%), Biological yield plant^{-1} (g) (96.36, 28.579%), Number of Compound leaves plant^{-1} (95.8, 49.928%), Harvest index (%) (95.2, 33.137%), Fresh weight of shoot plant^{-1} (g) (94.8, 41.01%), Plant height at maturity (cm) (94.2, 34.20%), Tuber yield plant^{-1} (kg) (93.6, 34.42%), Plant emergence (%) (92.5, 24.22%), Unmarketable tubers yield plant^{-1} (kg) (91.7, 43.23%), and Number of tubers plant^{-1} (68.8, 26.32%) in Exhibit high heritability & GA. Similar result were recorded for plant height and number of tuber plant^{-1} by Prajapati *et al.* 2020 [14], Tripura *et al.* 2016 [21], Patel *et al.* (2017) [12] for number of tuber per plant; Mishra *et al.* (2017) [10] for tuber yield per plant, Panigrahi and Pradhan (2017) [11] for harvest index. High values of heritability in broad sense are helpful in identifying the appropriate character for selection and in enabling the breeder to select superior genotypes on the basis of phenotypic expression and its utilization in future breeding programme.

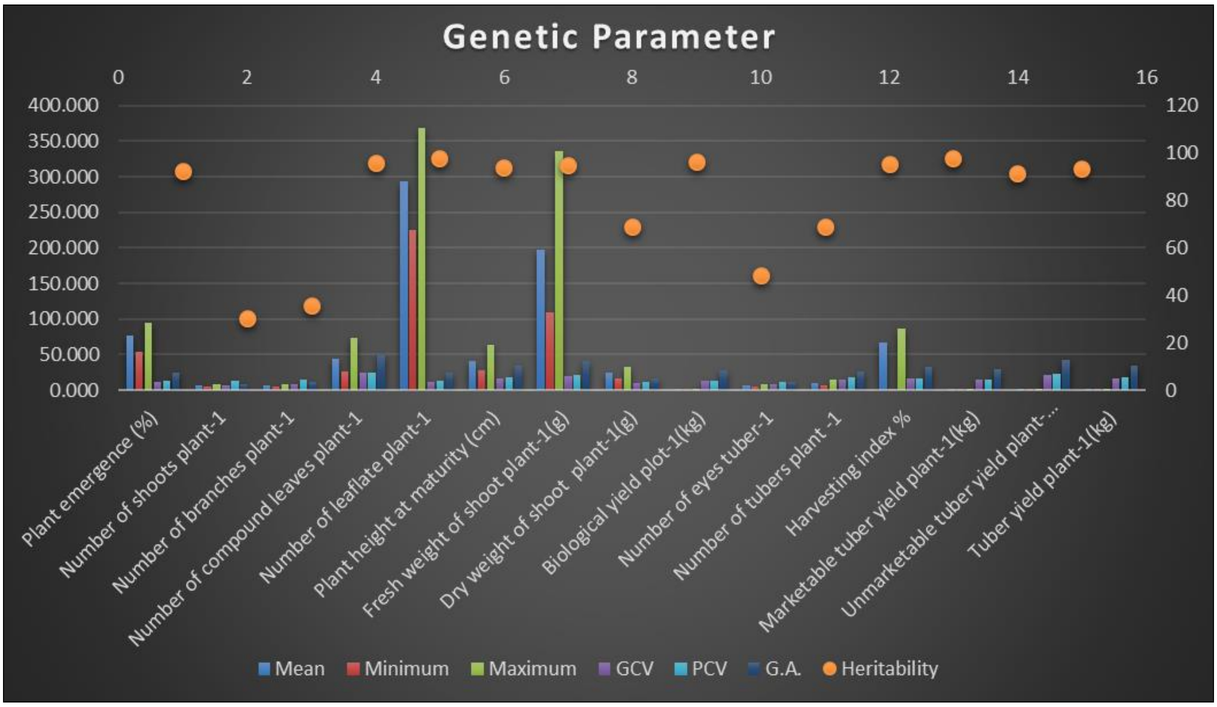

Fig 1: Genetic parameters of variation for tuber yield and its component traits in potato genotypes

Table 3: Genetic parameters of variation for tuber yield and its component traits in potato genotypes

Characters	Mean	Minimum	Maximum	GCV	PCV	Heritability	G.A.
Plant emergence (%)	76.882	54.7567	94.8967	12.227	12.713	92.5	24.226
Number of shoots plant^{-1}	6.792	5.46667	8.2	6.905	12.518	30.4	7.847
Number of branches plant^{-1}	6.612	4.53333	8.4	8.824	14.699	36	10.913
Number of compound leaves plant^{-1}	44.056	26.9833	74.3167	24.76	25.295	95.8	49.928
Number of leaflate plant^{-1}	292.992	224.873	368.06	12.422	12.549	98	25.329
Plant height at maturity (cm)	40.648	27.834	64.4633	17.103	17.617	94.2	34.202
Fresh weight of shoot plant^{-1} (g)	197.615	108.846	336.539	20.454	21.011	94.8	41.017
Dry weight of shoot plant^{-1} (g)	24.144	16.2707	33.476	9.885	11.883	69.2	16.94
Biological yield plant^{-1} (kg)	0.131	0.10467	0.181	13.873	13.539	96.36	28.579
Number of eyes tuber^{-1}	6.172	5.20333	8.33333	7.859	11.298	48.4	11.262
Number of tubers plant $^{-1}$	9.208	6.6	14.5333	15.405	18.574	68.8	26.32
Harvesting index %	66.631	0.20633	87.4063	16.488	16.9	95.2	33.137
Marketable tuber yield plant^{-1} (kg)	0.222	0.13567	0.31833	14.193	14.423	97.83	29.238
Unmarketable tuber yield plant^{-1} (kg)	0.478	0.32333	0.72667	21.92	22.895	91.7	43.233
Tuber yield plant^{-1} (kg)	0.700	0.50587	0.9872	17.27	17.849	93.6	34.421

Note: kg= Kilogram, cm=centimeter, g=gram

Distribution of Genotypes in to Cluster

Fifty genotypes were clustered into six, different clusters on the basis of D² statistics. Clustering pattern of Germplasm lines of potato are depicted in table no. 4 and Fig 2. Among the six clusters formed, cluster I had maximum number of genotypes (42) followed by cluster V (3 genotypes) cluster II (2 genotypes). These clustering pattern help in identifying distinct genetic groups and understanding the genetic diversity within a breeding population. Distribution of genotypes into different cluster suggested that of genetic diversity among genotypes & indicating that material may serve as a good source for selecting the diverse parents for hybridization program and aimed to isolate desirable recombinant for yield as well as other character. Sahu *et al*. (2014) [19].

Table 4: Clustering arrays of Potato genotypes

Cluster	No of Genotypes	Names of Genotypes
I	42	AICRP-P-78, AICRP-C-6, AICRP-C-13, AICRP-P-42, AICRP-C-17, AICRP-C-20, AICRP-C-14, AICRP-P-85, 2020 IGP-1, 2020 IGP-2, 2020 IGP-3, 2020IGP-4, 2020 IGP -6, 2020 IGP -7, 2020IGP–8, 2020IGP-9, 2020 IGP-10, K. Surya, K. Jyoti, K. Sinduri, K. Lalit, K. Mohan, K. Neelkanth, K. Khyati, KCH-1, K. Ashoka, K. Garima, K. Arun, K. Lalima, K. Lima, AICRP-P-45, AICRP-P-46, AICRP-P-53, AICRP-P-73, AICRP-P-21, 2022 IGP-1, 2022 IGP-2, 2022 IGP- 3, 2022 IGP- 6, 2022 IGP- 7, 2022 IGP-8 and 2022 IGP- 9
II	2	AICRP-P-48 and 2022 IGP-4
III	1	AICRP-C-5
IV	1	2020 IGP-5
V	3	KCH-3, K. Himalni and 2022IGP-10
VI	1	2022IGP-5

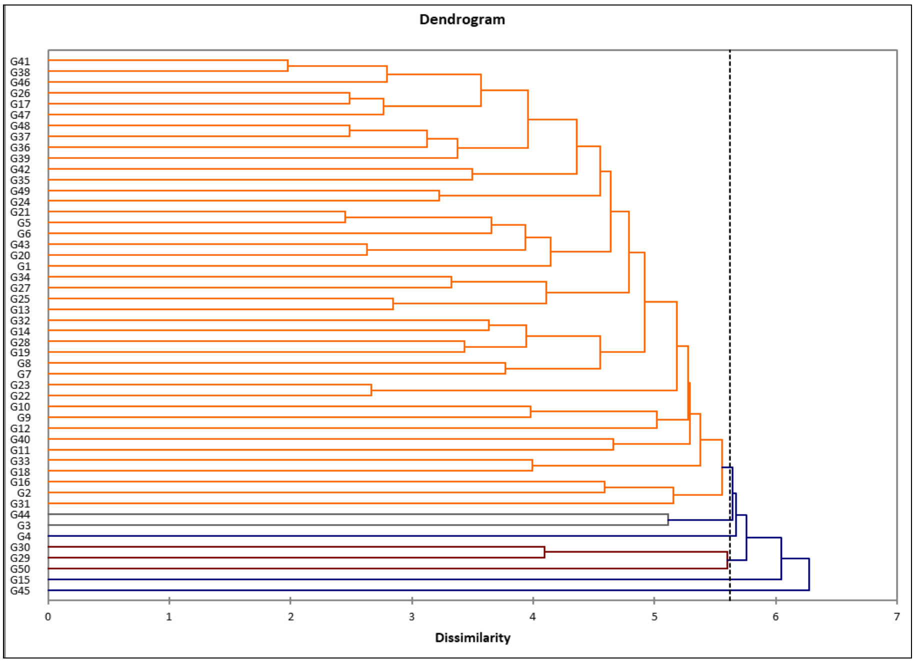

Fig 2: Dendrogram dissimilarities between clusters of Potato genotype

Inter Cluster Distances

The average intra and inter cluster distances are derived from D^2 values. It is assumed that the statistical distance (D) is the index of genetic diversity. Table No. 5 represents the average D^2 values of intra and inters cluster distances of potato genotypes under study. The inter cluster distances varied from 35.453 to 153.050. The highest inter cluster distances (D^2) was reported between Cluster III and V (153.050) followed by V and VI (112.8395), III and IV (109.235), I and III 107.9085, II and V (88.580) and lowest between cluster I and IV (35.453). The intra cluster distances ranged from 17.630 to 36.778. The highest intra cluster distances was observed cluster II (36.00) and minimum (17.630) for cluster I. The distances between two clusters indicate the degree of diversification. Greater distances between clusters signify greater divergence, while shorter distances indicate lesser divergence. Large cluster distances suggest that the genotypes within these clusters have significant genetic differences, whereas shorter intra-cluster distances indicate that the genotypes are relatively genetically close. Clusters with maximum inter cluster distances were found to be highly divergent groups. Hence inter cluster distances must be taken in future hybridization programme. It assume that maximum amount of heterosis is manifested in cross combination involving the genotypes belonging to must divergent clusters.

Table 5: Average intra and Inter cluster distances of D^2 potato genotypes related to yield attributing trait

Clusters	I	II	III	IV	V	VI
I	17.6305	36.7786	107.9085	35.4534	55.5627	64.5190
II		36.0057	75.5716	48.9647	88.5802	38.6383
III			0	109.2351	153.0504	59.2729
IV				0	62.8904	73.5841
V					32.1578	112.8395
VI						0

Mean performances of all the characters in different cluster is present in Table 6. The result obtained from cluster means for different characters showed potential variation present among clusters. Highest cluster mean reported for number of total leaflets plant^{-1} (326.72) and lowest for biological yield plant^{-1} (g). The genotypes in the cluster V had maximum number of total leaflets plant^{-1}, fresh weight of shoot plant^{-1} (g), dry weight of shoot plant^{-1} (g), number of eyes tuber-1, number of tubers plant^{-1} and unmarketable tuber yield plant^{-1} (kg). Considerable amount of marketable tuber yield plant^{-1} (kg), Harvest index (%) and tuber yield plant^{-1} (kg) was observed by the cluster IV. Cluster III and VI for number of compound leaves plant^{-1}, Plant emergence (%) and Number of branches plant^{-1}, Plant height at maturity (cm) respectively reported. These genotypes hold significant promise as parental stock for creating genetic variability for selection and as suitable donors for these traits in hybridization programs. By hybridizing these genotypes, we can generate genetic variability that can be harnessed for selection purposes.

Number of compound leaves plant^{-1} contributed to maximum towards genetic divergences, followed by Fresh weight of shoot plant^{-1} (g), Plant height at maturity (cm) and number of tubers plant^{-1}. These characters were considered to be most important for the genetic diversity. Lowest contribution was made by number of eyes tuber^{-1} (Table No. 6).

Table 6: List of character with contribution percentage

Characters	Contribution (Percent)
PE (%)	5.98
NSPP	4.66
NBPP	5.01
NCLPP	12.3
NTLPP	5.99
PH (cm)	8.71
FWSPP(g)	10.42
DWSPP(g)	4.92
BYPP(g)	5.92
NEPT	4.55
NTPP	7.67
UMTYPP(g)	6.56
MTYPP(g)	6.78
HI (%)	5.4
TYPP	5.29

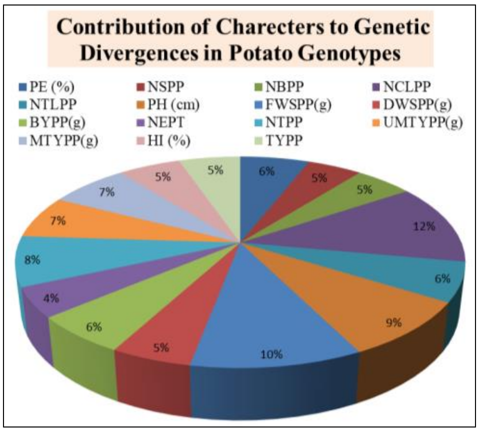

Fig 3: Contribution of Characters to Genetic Divergences in Potato Genotypes

Table 7: Cluster mean value for different characters in potato Genotypes

Cluster	PE (%)	NSPP	NBPP	NCLPP	NTLPP	PH (cm)	FWSPP(g)	DWSPP(g)	BYPP	NEPT	NTPP	UMTYPP	MTYPP	HI (%)	TYPP
I	77.3162	6.6434	6.4779	42.7167	292.2159	39.1765	200.8185	23.6245	0.1310	6.0750	9.1825	0.2239	0.4038	67.6594	0.6277
II	68.1350	8.2000	7.1667	46.9933	273.6300	42.2383	172.0333	26.4503	0.1693	6.1633	9.4167	0.1849	0.3833	60.1936	0.5683
III	83.6867	5.3333	5.6667	66.5800	244.6267	56.1825	108.8460	27.2627	0.1443	5.4100	11.2667	0.1969	0.4267	66.6881	0.6236
IV	64.8100	7.4667	6.8000	41.4100	313.3633	35.8213	182.6037	25.1933	0.1447	6.3000	7.3333	0.2387	0.5567	85.0324	0.7953
V	81.9444	7.3333	7.3333	58.1533	326.7267	50.8927	236.7687	27.7924	0.1141	6.8667	11.6956	0.2954	0.4503	81.1236	0.7458
VI	82.9333	6.3000	8.4000	32.0400	263.7433	64.4633	151.0720	23.4907	0.1197	5.7333	8.1333	0.1849	0.3533	58.3168	0.5382

Note: PE =Plant emergence(%), NSPP=Number of shoots plant^{-1}, NBPP=Number of branches plant^{-1}, NCLPP=Number of Compound leaves plant^{-1}, NTLPP=Number of total leaflets plant^{-1}, PH=Plant height at maturity(cm), FWSPP=Fresh weight of shoot plant^{-1}, (g) DWSPP=Dry weight of shoot plant^{-1} (g), BYPP = Biological yield plant^{-1} (kg), NEPT=Number of eyes tuber^{-1}, NTPP=Number of tubers plant^{-1}, UMTYPP=Unmarketable tuber yield plant^{-1} (g), MTYPP=Marketable tuber yield plant^{-1} (kg),HI =Harvest index(%) and TYPP=Tuber yield plant^{-1} (kg)

Conclusion

The phenotypic coefficient of variance (PCV) was slightly higher than the genotypic coefficient of variance (GCV) for all the characters studied, suggesting that the variation is influenced not only by genotypes but also by the environment to some extent. The estimation of high heritability with high genetic advance percent of mean for number of total leaflets plant^{-1}, marketable tuber yield plant^{-1} (kg), biological yield plant^{-1} (g), number of compound leaves plant^{-1}, harvest index (%), fresh weight of shoot plant^{-1} (g), plant height at maturity (cm), tuber yield plant^{-1} (kg), plant emergence (%), unmarketable tubers yield plant^{-1} (kg), dry weight of shoot plant^{-1} (g) and number of tubers plant^{-1} indicates that these characters are governed by additive gene effects and are less influenced by the environment. Therefore, selecting for these traits, if they are positively associated with yield, will be beneficial for improving potato. Conversely, for characters with low genetic advance as a percentage of the mean, hybridization or heterosis breeding may be exploited for their improvement. Based on this clustering, it can be concluded that an effective hybridization program can be initiated by including genotypes from diverse groups. This approach can produce superior segregants, which can be used to develop high-yielding potato varieties in the future. Superior genotype selected from different clusters can be use future crossing programme *viz* 2020- IGP-4 from cluster I, P-48 and 2022-IGP-4 in cluster II, C-5 from Cluster-III, 2020-IGP-5 from IV cluster, Kufri Himalni and 2022-IGP-5 from Cluster V and VI respectively.

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